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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Jul 22 15:27:41 1998; MasPar time 12.38 Seconds 767.369 Million cell updates/sec Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-915-659A-7 (1-260) from US08915659A.pep 1943 1 MGRPRPRAAKTWMFLLLLGG......VYTNICRYLDWIKKIIGSKG 260

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Mean 42.128; Variance 70.703; scale 0.596 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	0.00e+00	3.84e-170	5.44e-164	5.23e-163	8.52e-161	2.43e-158	7.53e-158	2.33e-157	7.22e-157	3.60e-154	3.60e-154	6.33e-154	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153	1.11e-153
Description	neuropsin - mouse	serine proteinase SCC	trypsin (EC 3.4.21.4)		Trypsin complexed wit	\rightarrow		trypsin (EC 3.4.21.4)	beta-trypsin (EC 3.4.														
QI	156559	A53968	TRDG	S31779	TRDGC	TRBOTR	A27547	TRRIZ	1TGSZ	2TLDE	B25528	TRRI	lTPS	1TYN	1JRTA	1JRSA	1TGB	1TGT	4TPIZ	2PTN	1TPP	1TPO	1BTY .
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% Query Match Length DB	260	253	247	238	246	229	247	246	225	223	246	246	223	223	223	223	223	223	223	223	223	223	223
% Query Match	9.92	42.9	41.6	41.4	40.9	40.4	40.3	40.2	40.1	39.5	39.5	39.2	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4
Score	1488	833	808	804	795	785	783	781	779	768	768	167	166	166	166	992	166	166	166	166	166	992	992
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241 VYTNICRYLDWIKKIIGSK 259

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beta-trypsin (EC 3.4. trypsin (EC 3.4.21.4) beta-trypsin (EC 3.4.21.4) beta-trypsin (EC 3.4.21.4) repsin (EC 3.4.21.4) repsin (EC 3.4.21.4) beta-trypsin (EC 3.4.21.4) beta-trypsin (EC 3.4.21.4) trypsin (EC 3.4.21.4)	
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1-247 ##label PIN

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75,77,80,85
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#authors
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Matches
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                                   KEYWORDS
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#journal Mol. Cell. Biol. (1985) 5:2669-2676
#title Differential regulation of trypsinogen mRNA translation:
full.length mRNA sequences encoding two oppositely charged
#cross-references MUID:86284628
#accession A26273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQPNDPGVYTQVCKFTKW 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCKMNEYTVHLGSDTLGDR--RAQRIKASKSFRHPGY-ST--QTHVNDLMLVKLNSQARL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ILLLSLALETAGEE-AQGDKIIDGAPCARGSHPWQVALLSGNQLHCGGVLVNERWVLTAA 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trypsin (EC 3.4.21.4) precursor, anionic - dog cationic trypsinogen #formal_name Canis lupus familiaris #common_name dog 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jul-1997
                                                                                                  #formal_name Homo sapiens #common_name man
07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change
08-Sep-1997
                                                                                                                                                                                        Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt,
Carlstein, A.; Egelrud, T.
J. Biol. Chem. (1994) 269:19420-19426
Cloning, expression, and characterization of stratum con
chymotryptic enzyme. A skin-specific human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain trypsin homology #label TRY
th 253 #molecular-weight 27525 #checksum 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 833; DB 2; Length 253;
Pred. No. 3.84e-170;
44; Mismatches 77; Indels
                                                  A53968 #type complete
serine proteinase SCCE precursor - human
stratum corneum chymotryptic enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GDB:377730
#map_position 7q35-7q35
CLASSIFICATION #superfamily trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                      1-253 ##label HAN
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                                                                                                                                                                                                                                                                                                               **status preliminary ##molecule_type mRNA
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Best Local Similarity 47.3%;
Matches 116; Conservative
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#label Sig\
#domain activation peptide #status predicted #label APT\
#product trypsin III #status predicted #label MAT\
#domain trypsin homology #label TRY\
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#domain activation peptide #status predicted #label APT\
#product trypsin, anionic #status predicted #label ENZ\
#domain trypsin homology #label TRY.
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*superfamily trypsin; trypsin homology
hydrolase; pancreas; protein digestion; serine proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 NARVATISLPRACAAPGTQCLISGWGNTLSSGTNYPELLQCLDAPILTQAQCEASYPGQI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TENMICAGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGYG-CAQKNKPGVYTKVCNFVDW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 HCYKSRIQVRLGEYNIDVLEGNEQFINSAKVIRHPNYNSW-ILD-N-DIMLIKLSSPAVL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LILAFLGAA-VATPIDDDDKIVGGYTCEENSVPYQVSLNAGYHF-CGGSLISDQWVVSAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Salmo salar #common_name Atlantic salmon 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 07-Nov-1997 86667; S31779 S66657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #disulfide_bonds #status predicted\
#active_site His, Asp, Ser #status predicted\
#binding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 247 #molecular-weight 26423 #checksum 8431
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trypsin (EC 3.4.21.4) III precursor - Atlantic salmon
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#active_site His, Asp, Ser #status predicted
#length 238 #checksum 6737
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Eur. J. Biochem. (1995) 232:677-685
Molecular cloning and characterization of anionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 247;
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Pred. No. 5.44e-164;
57; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.68;
44.28;
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30-160,48-64,
132-233,139-206,
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16-238
16-231
22-152,40-56,
124-225,131-198,
163-177,188-212
55,99,192 #le:
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115-216,122-189,
154-168,179-203
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7-131,132-229
6-7
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#domain activation peptide #status predicted #label APT\
#product trypsin, cationic #status predicted #label ENZ\
#domain trypsin homology #label FRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Pinsky, S.D.; LaForge, K.S.; Scheele, G.
#journal Mol. Cell. Biol. (1985) 5:2669-2676
#title Differential regulation of trypsinogen mRNA translation:
full-length mRNA sequences encoding two oppositely charged
trypsinogen isoenzymes in the dog pancreas.
#cross-references MUID:86284628
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                                                                                                                                                            120 LPSSCASSGTRCLVSGWGNLSGSSSNYPDTLRCLDLPILSSSSCNSAYPGQITSNMFCAG 179
                                                                                                                                                                                                                                            141 LADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
                                                                                                                                                                                                                                                                              180 FMEGGKDSCQGDSGGPVVCNGQLQGVVSWGYG-CAQRNKPGVYTKVCNYRSWISSTMSSN 238
                                                                                                                                                                                                                                                                                                  201 SSKGA-DICQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKIIGSK 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 ATLNSRVSAIALPKSCPAAGTQCLISGWGNTQSIGQNYPDVLQCLKAPILSDSVCRNAYP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 ASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYP 189
                                                                                                                                        63 VRLGEHNIAVNEGTEQFIDSVKVIMHPSYNSRNL-D-N-DIMLIKLSKPASLNSYVSTVA 119
                                                                                        4 AFAAPIDDEDDKIVGGYECRKNSASYQASLQSGYHF-CGGSLISSTWVVSAAHCYKSRIQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTFIFLALLGAT-VAFPIDDDDKIVGGYTCSRNSVPYQVSLNSGYHF-CGGSLINSQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 KTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVL 69
                                                                                                                                                                                                                                                                                                                                                                     trypsin (EC 3.4.21.4) precursor, cationic - dog cationic trypsinogen #formal_name Canis lupus familiaris #common_name dog 30.589-1987 #sequence_revision 30-Sep-1987 #text_change
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Pred. No. 8.52e-161;
58; Mismatches 80; Indels
   Length 238;
                                  68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #disulfide_bonds #status predicted\
Score 804; DB 2; Le
Pred. No. 5.23e-163;
56; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -246 ##label PIN
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Best Local Similarity 42.2%;
Matches 106; Conservative
A1.4%;
Similarity 45.8%;
110; Conservative
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0-160,48-64,
32-233,139-206,
171-185
                                    110;
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75,77,80,85
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Query Match
Best Local S.
Matches 11
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REFERENCE
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#journal J. Mol. Biol. (1975) 98:693-717
#title The refined crystal structure of bovine beta-trypsin at 1.8
#cross-references MID:76072097
#contents annotation; X-ray crystallography; binding sites for calcium, substrate, and inhibitors
MENT Trypsinogen is synthesized in the acinar cells of the pancreas.
MENT Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal hexapeptide. Subsequent cleavage after Lys-131 leads to alpha-trypsin. Further cleavage after Lys-176
yields pseudotrypsin. A cleavage may also occur after Arg-105.
SSIFICATION #superfamily trypsin, trypsin homology
WORDS hydrolase; pancreas; protein digestion; serine proteinase;
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#product alpha-trypsin #status experimental #label MPT\
#cleavage_site Lys-Ile (enteropeptidase) #status
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#domain activation peptide #status experimental #label
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190 GQITDGMYCAGSSKGA-DTCQGDSGGPLYCDGALQGITSWGSDPCGRSDKPGVYTNICRY 248
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#binding_site calcium (Glu, Asn, Val, Glu) #status
experimental\

                                                                                                                                                                                                                                                                                                                  #formal_name Bos primigenius taurus #common_name cattle 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
#journal Biochem. Biophys. Res. Commun. (1966) 24.346-352
#title Covalent structure of bovine trypsinogen. The position remaining amides.
#cross-references MUID:67168848
#accession A90164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type protein
##residues 1-57,'Q',59-67,'Q',69-150,'N',152-176,'N',178-229
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Biochemistry (1975) 14:1358-1366
Amino acid sequence of dogfish trypsin.
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#length 229 #molecular-weight 23993 #checksum
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Pred. No. 2.43e-158;
50; Mismatches 68;
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annotation; revisions
the sequence agrees with that shown
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A90164
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Philos. Trans. R. Soc.
annotation; revisions
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Best Local Similarity 46.6%;
Matches 108; Conservative
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                                                          62 NVVEGNEQFISASKSIVHPSYNSNTL-N-N-DIMLIKLKSAASLNSRVASISLPTSCASA 118
                                                                          GTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDS 178
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                                                                                                                                           149 GOKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGSSKGA-DT 207
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       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trypsin (EC 3.4.21.4) precursor, cationic - rat #formal_name Rattus norvegicus #common_name Norway rat 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change A27547
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#binding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 247 #molecular-weight 26269 #checksum 9664
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    3 DDDKIVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNI
                     ##residues 1-247 ##label FLE ##cross-references GB:M16624; NID:g206498; PID:g206499 FICATION #superfamily trypsin; trypsin homology calcium binding; hydrolase; protein digestion; serine
                                                                                                                                                                      179 CQGDSGGPVVCSGKLQGIVSWGSG-CAQKNKPGVYTKVCNYVSWIKQTIASN 229
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Pred. No. 7.53e-158;
55; Mismatches 82; Indels
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pst Local Similarity 43.0%;
ches 108; Conservative
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LDWIKKIIGSK 259
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133-234,140-207,
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64,108,201
76,78,81,86
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RESULT

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#domain signal sequence #status predicted #label SIG\
#domain activation peptide #status predicted #label APT\
#product trypsin II #status predicted #label ENZ\
#domain trypsin homology #label TRY\
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hydrolase; pancreas; protein digestion; serine proteinase;
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trypsin (EC 3.4.21.4) precursor (with pancreatic secretory
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                                                                        #formal_name Norway rat
05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change
18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #active_site His, Asp, Ser #status predicted\
#binding_site calcium (Glu, Asn, Val, Glu) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors MacDonald, R.J.; Stary, S.J.; Swift, G.H.
#journal J. Biol. Chem. (1982) 257:9724-9732
#title Two similar but nonallelic rat pancreatic trypsinogens.
Nucleotide sequences of the cloned cDNAs.
#cross-references MUID:82265624
                                                                                                                                                                                                        #authors Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacD
R.J.; Rutter, W.J.
#journal J. Biol. Chem. (1984) 259:14255-14264
#title Structure of two related rat pancreatic trypsin genes.
#cross-references MUID:85054880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 VKLNARVATVALPSSCAPAGTQCLISGWGNTLSSGVNEPDLLQCLDAPLLPQADCEASYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKITDNMVCVGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGYG-CALPDNPGVYTKVCNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted
#length 246 #molecular-weight 26243 #checksum 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sidues 9-246 ##label MAC
The trypsin II mRNA is present in much lower quantities
trypsin I mRNA.
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Pred. No. 2.33e-157;
56; Mismatches 81; Indels
TRRT2 #type complete
trypsin (EC 3.4.21.4) II precursor - rat
trypsinogen II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #disulfide_bonds #status predicted\
                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-246 ##label CRA
SNCE A00948
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Best Local Similarity 42.6%;
Matches 107; Conservative
                                                                                                                                                            A22657; A00949
A22657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
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LDWIKKIIGSK
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132-233,139-206,
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                                                         ALTERNATE_NAMES
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136-141,116-120,
179-183,186-193,
204-209,159-163
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214-223
7-137,25-41,
109-210,116-183,
148-162,173-197
84,40,177
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46-50,63-67
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Matches
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                                                                                    Marguart, M.; Papamokos, E.; Huber, R. submitted to the Brookhaven Protein Data Bank, September 1982 cross-references PDB:1TGS
                                                                                                                                                                        Marquart, M.; Papamokos, E.; Huber, R.
J. Mol. Biol. (1982) 162:839

Three-dimensional structure of the complex between pancreatic secretory inhibitor (kazal type) and trypsinogen at 1.8 angstroms resolution. structure solution, crystallographic refinement and preliminary structural interpretation.
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6
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irreg.)\
#region helix (right hand 3-10) (contiguous with h3)\
#region helix (right hand alpha) (contiguous with h2)\
#disulfide_bonds\
#disulfide_bonds\
#disulfide_bonds\
#disulfide_bonds\
                                                                                                                                                                                                                                                                                                                    Acta Crystallogr. (1983) B39:480
The geometry of the reactive site and of the peptide groups
in trypsin, trypsinogen and its complexes with inhibitors.
TW005562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2TLDE #type complete trypsin (EC 3.4.21.4) (with mutant streptomyces subtilisin
                                                                                                                                                                                                                                                                                                                                                                                                                           in Atlas of Protein Sequence and Structure (Data Section), Dayhoff, M.O., ed., vol. 5, pp.105, National Biomedical Research Foundation, Silver Spring, Md., 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 VEGNEQFISASKSIVHPSYNSNTL-N-N-DIMLIKLKSAASLNSRVASISLPTSCASAGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dayhoff, M.O. in Atlas of Protein Sequence and Structure, Supplement 1, Dayhoff, M.O., ed., vol. 5, pp.88, National Biomedical Research Foundation, Silver Spring, Md., 1973
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trypsin inhibitor), chain Z - bovine #formal_name Bos primigenius taurus #common_name cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                       Guarneri, M.;
                                                                                                                                                             Bolognesi, M.; Gatti, G.; Menegatti, E.; Guarneri, M.;
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                                  pancreas
A50955
Bolognesi, M.; Gatti, G.; Menegatti, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination: X-ray diffraction hydrolase; serine proteinase
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216-225
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118-185
150-164
175-199
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TITLE

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#region beta sheet\
#region helix (right hand alpha) (single alpha turn,rest
                                                                       #authors Mitsui, Y.; Takeuchi, Y.; Nonaka, T.; Nakamura, K.T.
#submission submitted to the Brookhaven Protein Data Bank, September 1991
#cross-references PDB:2TLD
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Muclaic Acids Res. (1986) 14:8307-8330
Sequence organisation and transcriptional regulation of the mouse elastase II and trypsin genes.
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hand alpha) (contiguous with h2)\
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Refined crystal structure of the complex of subtilisin Bi and streptomyces subtilisin inhibitor at 1.8 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVVE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 VLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKD 92
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trypsin (EC 3.4.21.4) precursor - mouse
#formal_name Mus musculus #common_name house mouse
30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4407
Crystal structure of an engineered subtilisin inhibitor
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inhibitor), chain E - bovine
#formal_name Bos primigenius taurus #common_name
A50948
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#active_site Asp, His, Ser #label CAT\
#site #label 13
#length 223 #molecular-weight 23071 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 SGGPLVCDGALQGITSWGSDPCGRSDRPGVTTNICRYLDWIKKIIGSK 259
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Pred. No. 3.60e-154;
48; Mismatches 68;
                                                                                                                                                                                                                                                                     complexed with bovine trypsin. TN005551
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#region helix (right
#region helix (right
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#region beta sheet\
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Local Similarity 46.5%;
les 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              resolution.
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#authors
#journal
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1-246 ##label MAC
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Best Local Similarity 42.3%;
Matches 105; Conservative
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A67200
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24-239
30-160,48-64,
132-233,139-206,
   ##residues
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CLASSIFICATION
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J. Biol. Chem. (1984) 259:14255-14264
Structure of two related rat pancreatic trypsin genes.
                                                                                                                                                                #domain signal seguence #status predicted #label SIG\
#product trypsin #status predicted #label MAT\
#domain trypsin homology #label TRY\
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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#binding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 246 #molecular-weight 26203 #checksum 5833
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trypsin (EC 3.4.21.4) I precursor - rat
trypsinogen I
#formal_name Rattus norvegicus #common_name Norway rat
17-bec-1882 #sequence_revision 17-bec-1882 #text_change
20-mar-1998
B22657; A00948
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#journal J. Biol. Chem. (1982) 257:9724-9732
#title Two similar but nonallelic rat pancreatic trypsinogens.
#cross-references MUD:82265624
                          ##molecule_type mRNA
##residues 1-246 ##label STE
##cross-references GB:X04574; NID:954918; PID:954919
##cross-references GB:X04574; NID:954918; PID:954919
IFICATION #superfamily trypsin, trypsin homology
RDS calcium binding; hydrolase; protein digestion; serine
                                                                                                                                                                                                                                                                                                                                                                                                           7;
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Pred. No. 3.60e-154;
56; Mismatches 79; Indels
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##cross-references GB:J00778; NID:9206508; ##note the codon ATC for
##note Leu and GAC for residue 170 as Asn
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#accession B22657
#cross-references MUID:87066713
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St Local Similarity 42.7%;
(tches 106; Conservative
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##molecule_type mRNA
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132-233,139-206,
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63,107,200
75,77,80,85
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#domain signal sequence #status predicted #label SIG\
#domain activation peptide #status predicted #label APT\
#product trypsin I #status predicted #label ENZ\
#domain trypsin homology #label TRY\
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*submission submitted to the Brookhaven Protein Data Bank, September 1994
#cross-references PDB:1TPS
ERENCE IN023754
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#region helix (right hand 3-10) (contiguous with h3)\
#region helix (right hand alpha) (contiguous with h2)\
#disulfide_bonds\
#disulfide_bonds\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atomic structure of the trypsin-a90720a complex: a unified approach to structure and function.
14/1; 67/2; 152/1; 197/3
#superfamily trypsin; trypsin homology
hydrolase; pancreas; protein digestion; serine proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 TSSMICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWGYG-CALPDNPGVYTKVCNFVGW 238
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#active_site His, Asp, Ser #status predicted\
#binding_site calcium (Glu, Asn, Val, Glu) #status
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Trypsin complexed with inhibitor a90720a - bovine
#formal_name Bos primigenius taurus #common_name
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 767; DB 1; Length 246; Pred. No. 6.33e-154; 56; Mismatches 80; Indels
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#length 246 #molecular-weight 25959
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Determination: X-ray diffraction
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Search completed: Wed Jul 22 15:28:54 1998 Job time: 73 secs.
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#region helix (right hand 3-10) (contiguous with h3)\
#region helix (right hand alpha) (contiguous with h2)\
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J. Am. Chem. Soc. (1993) 115:12619
Atomic structure of the trypsin-cyclotheonamide a complex: lessons for the design of serine protease inhibitors.
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                                                                            1 IVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVE 59
                                                                                                    33 VLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKD 92
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Beta trypsin complexed with cyclotheonamide a - bovine
#formal_name Bos primigenius taurus #common_name cattle
A67202
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 Length 223;
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 Score 766; DB 5; Length 223
Pred. No. 1.11e-153;
48; Mismatches 68; Indels
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Determination: X-ray diffraction
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Query Match 39.4%;
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Matches 106; Conservative
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Authors Kurinov, I.V.: Harrison, R.W.
*submission submitted to the Brookhaven Protein Data Bank, February 1996
*cross-references PDB:1JRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 LISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 VLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAACKKPYTVRLGDHSLQNKD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVE 59
                                                                                                                                                                                                                                                                                                                     digestion; hydrolase; pancreas; serine protease; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #disulfide_bonds\
#disulfide_bonds\
#disulfide_bonds
#length 2233 #molecular-weight 23305 #checksum 7159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
6
1JRTA #type complete
trypsin (EC 3.4.21.4), chain A - bovine
hemiacetal complex between leupeptin and trypsin
fromal_name Bos taurus: #common_name bovine
                                                                                                                                                                                        Kurinov, I.V.; Harrison, R.W.
Nat. Struct. Biol. (1994) 1:735
Prediction of new serine proteinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 SGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 766; DB 5; Length 223
Pred. No. 1.11e-153;
48; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 SGGPVVCSGKLQGIVSWGSG-CAQKNKPGVYTKVCNYVSWIKQTIASN 223
                                                                                                                                                                                                                                                                                                                                                             #region helix (right hand 3-10)\
#region helix (right hand alpha)\
#region helix (right hand 3-10)\
                                                                                                                                                                                                                                                        Resolution: 1.8 angstroms
Determination: X-ray diffraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #region beta sheet\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta sheet\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #region beta sheet
#disulfide_bonds/
#disulfide_bonds/
#disulfide_bonds/
                                                                                                                                                                                                                                                                                                    R-value: no refinement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a 39.48;
Similarity 46.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 46.5%;
les 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                              145-151
209-211
63-66,47-50,15-19,
23-31,34-37,86-90,
67-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136-141,115-120,
180-183,186-193,
204-208,160-163
                                                                                                                             #submission
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Best Local
                                                                                                                                                                                          #authors
#journal
                                                                                     REFERENCE
#authors
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116-183
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173-197
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                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                      #title
                                     PDB_TITLE
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FEATURE
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                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                 39-41
                                                                                                                                                                                                                                                                           COMMENT
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 15.26 Seconds 717.292 Million cell updates/sec Wed Jul 22 15:29:54 1998;

not generated. abular output

>US-08-915-659A-7 (1-260) from US08915659A.pep 1943 1 MGRPRPRAAKTWMFLLLLGG.......vyTNICRYLDWIKKIIGSKG 260 Title: Description: Perfect Score:

PAM 150 Gap 11 Scoring table: Sequence:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb15 Database:

1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

scale 0.712 Variance 59.229; Mean 42.195; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Pred. No.	0.00e+00	1.15e-206	5.59e-187	2.06e-181	1.55e-180	1.17e-179	1.17e-179	2.30e-179	1.31e-177	7.44e-176	1.12e-167	1.23e-165	1.23e-165	5.14e-163	5.33e-154	7.73e-153	1.73e-148	1.62e-139	9.53e-134	6.97e-133	
Description	SERINE PROTEASE INHIBI	PROTEASE M PRECURSOR.	NES1-NORMAL EPITHELIAL	TRYPSIN PRECURSOR (EC	TRYPSINGEN (FRAGMENT)	TRYPSINGGEN A2 PRECURS	TISSUE KALLIKREIN.	TRYPSINGEN A3 PRECURS	TRYPSINGEN B2 PRECURS	TRYPSINGEN B1 PRECURS	TRYPSINGEN IV B-FORM.	KALLIKREIN PRECURSOR.	KALLIKREIN PRECURSOR (KALLIKREIN (FRAGMENT).	PREPROTRYPSIN PRECURSO	KALLIKREIN (FRAGMENT).	TRYPSINGEN I (FRAGMEN	VENOM PLASMINOGEN ACTI	CALOBIN.	SERINE PROTEASE PRECUR	
Ω	061955	92876	099920	092099	091515	042158	261855	042608	042160	042159	015665	028773	029474	063275	092046	063274	091036	091516	091053	013060	
B	10	7	~	12	12	12	10	12	12	12	7	4	7	2	13	10	12	12	12	12	
Query Match Length	260	244	273	242	237	247	261	247	245	244	259	258	261	239	249	235	219	258	262	260	
Query	9.92	43.4	39.9	39.0	38.8	38.7	38.7	38.6	38.3	38.0	36.5	36.2	36.2	35.7	34.1	33.9	33.1	31.5	30.5	30.4	
Score	1488	843	116	757	754	751	751	750	744	738	710	703	703	694	663	629	644	613	593	290	
No.	1	7	т	4	S	ø	7	ω	თ	10	11	12	13	14	15	16	. 17	18	19	70	

241 VYTKICRYTTWIKKTMDNR 259

2.72e-130 1.02e-129 7.46e-129 3.96e-127	7866-11 1136-11 1136-11 1146-11 1146-11 1166-11	
SERINE PROTEASE PRECUR SERINE PROTEASE PRECUR GLANDULAR KALLIKREIN (CAPILLARY PERMEABILITY		PRECURSOR ADIPSIN. NATURAL KILLER CELL PR SERINE PROTESE PRECUR GRANZYME-LIKE PROTEIN LYMPHOCIYE MET-ASE 1 P CHYMOTRYPSIN BI (FRAGM NERVE GROWTH FACTOR, G SERINE PROTEASE HOMOLO HGF ACTIVATOR LIKE PRO
013059 013056 Q03955 042207	013063 091509 013057 013062 091508 091508 091510 091511 091511 091510 013058	061280 063636 013061 063224 008643 018487 012284 015358
12021	20222222222	770707070
258 260 250 258	255 255 255 255 255 255 255 255 255 255	258 260 260 271 135 560
9999	0,000,000,000,000	
581 579 576 570	500 500 500 500 500 500 500 500 500 500	509 504 502 476 476 473 4713
21 23 24	33 4 33 3 3 5 5 5 5 8 5 6 8 5 6 8 5 6 6 6 6 6 6 6 6	W W W A A A A A A V 80 00 0 11 4 12 14 14

ALIGNMENTS

61 VLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSNPEDHSHD 120 121 IMLIRLQNSANLGDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYS 180 ONKCERAYPGKITEGMVCAGSSNGADTCQGDSGGPLVCDGMLQGITSWGSDPCGKPEKPG 240 1 MGRPPPCAIQPWILLLERMGAWAGLTRAQGSKILEGRECIPHSQPWQAALFQGERLICGG 60 9 Gaps ZU-LIN C., YOSHIDA S., KATO K., MOMOTA Y., SUZUKI J., TANAKA T., ITO J., NISHINO H., AIMOTO S., KIYAMA H.;
J. NUBUROSCI. 15:5088-5097(1995).
EMBL; D30785; G1020091; -.
SERINE PROTEASE. 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SERINE PROTEASE INHIBITOR 5 (NEUROPSIN).
SPI5.
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ö Length 260; Score 1488; DB 10; Length 26 Pred. No. 0.00e+00; 38; Mismatches 34; Indels 260 AA; 28523 MW; 232F78DB CRC32; Æ 260 PRT; SEQUENCE FROM N.A. STRAIN-BALB/C; TISSUE-HIPPOCAMPUS; MEDLINE; 95348817. PRELIMINARY; / Match Local Similarity 72.2%; les 187; Conservative LT 1 Q61955 Q61955; Q1-NOV-1996 (01-NOV-1996 (SEQUENCE Query Match Best Loc Matches RESULT 음 ò 셤 ò g g ò οy

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Gaps

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Q92876 Q92876;

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57 SAAHCYKSRVEVRMGEHHIRVTEGKEQFISSSRVIRHPNYSSYNI-D-N-DIMLIKLSKP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||| |:: ||:||:| :: :| || |: : | || |:|: |
70 TAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCXNSSDVEDHNHDLMLLQLRDQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ATLNQYVQAVALPSSCAPAGTMCTVSGWGSTQSSSAD-GNKLQCLNIPILSDRDCDNSYP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 GMITDAMFCAGYLQGGKDSCQGDSGGPVVCNGELQGVVSWGYG-CAERDHPGVYAKVCLF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 EQLRRTTRSVVHPKYHQGSGPILPRRIDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWA-RVGDDHLLLLQG- 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RSLVFVLLIGAAFA----TEEDKIVGGKECSPYSQPHQVSLNSGYHF-CGGSLVNENWVV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-PYLORIC CAECA;
GENICOT S., RENTIER-DELRUE F., EDWARDS D., VAN BEEUMEN J., GERDAY
BIOCHIM. BIOPHYS. ACTA 1298:45-57(1996).
EMBL; X82223; G559508; -.
SIGNAL; HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARANOTOTHENIA MAGELLANICA.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
ACTINOPTERYGII; PERCIFORMES; NOTOTHENIOIDEI; NOTOTHENIIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 757; DB 12; Length 242;
Pred. No. 2.06e-181;
62; Mismatches 63; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                           Score 776; DB 2; Length 273;
Pred. No. 5.59e-187;
46; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST ASCUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOFATION UPDATE)
TRYPSIN PRECURSOR (EC 3.4.21.4) (ALPHA- AND BETA-TRYPSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKII 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 SDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVI 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29780 MW; 83E4135C CRC32;
                                                                                                                                                                                                             WATANABE K., BAND V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                 SEQUENCE FROM N.A.
MEDLLINE, 96320486.
LIU X.L., WAZEN D.E., WATANABE
CANCER RES. 56:3371-3379(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Query Match 39.9%;
Best Local Similarity 46.7%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.3%;
Matches 108; Conservative
                                                                                                                                                                                                                                                         66; G1835925;
273 AA; 29780
                            HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                   EMBL; S82666;
SEQUENCE 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 KTWMFLL-LLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKLMVVLSLIAAAWA-E--EQNKLVHGGP-CDKTSHPYQAALYTSGHLLCGGVLIHPLWV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 843; DB 2; Length 244;
Pred. No. 1.15e-206;
55; Mismatches 68; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAMASHIRO K., TSURUOKA N., KODAMA S., TSUJIMOTO M., YAMAMURA Y.,
TANAKA T., NAKAZATO H., YAMAGUCHI N.;
BIOCHIM. BIOPHYS. ACTA 1350:11-14(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ж.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-ALZHERHER'S DISEASE BRAIN TISSUE;
LITTLE S.P., JOHNSTONE E.M., DIXON E.P., NORRIS F., BUCKLEY W.,
BECKER G., JOHNSON M., DOBBINS J.R., WYRICK T., MILLER J.R.,
MACKELLAR W., HEPBURN D., CORVALAN J., MCCLURE D., LIU X.,
STEPHENSON D., CLEMENS J.;
J. BIOL. CHEM. 0.0-0(1997).
EMBL: 062801; G151878;
EMBL: D78203; G180493; -..
EMBL: AF013988; G2318115; -.
                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
ANISOWICZ A., SOTIROPOULOU G., STENMAN G., MOK S.C., SAGER
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
NESI-NORMAL EPITHELIAL CELL SPECIFIC GENE 1.
                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEASE M.
OCFCEFCE CRC32;
                                                                                                                                                       244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 PC
244 PF
26856 MW;
   241 VYTNICRYLDWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.8%;
Matches 118; Conservative
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01-FEB-1997 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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248 YLDWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                            PROTEASE M PRECURSOR
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MEDLINE; 97157069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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042608
042608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
ID Q61855
AC Q61855;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRVVVRLGEHNIRANEGTEQFISSSRVIRHPNYSSYNI-D-N-DIMLIKLSKPATLNQYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 QPVALPSSCAAAGTMCKVSGWGNTMSSTAD-RNKLQCLNIPILSDRDCENSYPGMITDAM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCAGYLEGGKDSCQGDSGGPVVCNNELQGVVSWGYG-CAERDHPGVYAKVCLFNDWLEST 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LIAAAYAA-PIDEDDKIVGGYECRKNSVAYQVSLNSGYHF-CGGSLVNENWVVSAAHCYK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
TRYPESINOGEN (FRAGMENT).
FUGU RUBRIPES (JAPANISE PUFFERFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; TETRAODONTIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠<u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 751; DB 12; Length 247;
Pred. No. 1.17e-179;
59; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 754; DB 12; Length 23'
Pred. No. 1.55e-180;
64; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                           WANG K., GAN L., LEE I., ROACH J., HOOD L.;
SUBMITIED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U25747; G971196; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011898; G2367495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRYPSINOGEN A2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D049AA4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                237 AA; 25726 MW; 6A296989 CRC32;
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                                                                                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN A2
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                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.8%;
Best Local Similarity 42.4%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.7%;
Best Local Similarity 42.0%;
Matches 105; Conservative
                                                                                                                            PRELIMINARY;
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247
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232 NDWL 235
                                         249 LDWI 252
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IGS 258
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                                                                                                      LT 5
Q91515
Q91515;
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042158
042158;
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124 LRLKKPADITDVVKPIDLPTEEPKLGSTCLASGWGSITPVKYEYPDELQCVNLKLLPNED 183
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                                                                                      63 HCYQTASRISVRIGEHNIFVNEGTEQQIQASKAIQHPQYNSWTI-D-N-DIMLIKLSSPA 119
                                                                                                                                                                            120 TLNQYAQAIALPSSCVNTGVMCTISGWGETQTSIGS-PDVLMCVQAPVLSDTSCRNSYPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 AHCHNDKYQVWLGKNNFLEDEPSAQHRLVSKAIPHPDFNMSLLNEHTPQPEDDYSNDLML 123
                                                                                                                                                                                                                                                                    179 DITNNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWGRG-CALPNYPGVYTKVCNYN 237
62
                       6 LFLALSLGGI-DAAPPVQ-SRIVGGFNCEKNSQPWQVAVYRFTKYQCGGILLNANWVLTA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LILALLVGVAAAAPYMYEDHIVGGSECAAHSQPWQVSLNIGYHF-CGGSLINSQWVVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TADA M., PETERS J., TAKAHASHI S., INOUE H., MIYAKE Y. SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; D10464; G520591; - - SEQUENCE 261 AA; 28775 MW; 509D1D00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 38.7%; Score 751; DB 10; L Local Similarity 42.4%; Pred. No. 1.17e-179; les 108; Conservative 57; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, TRYPSINGEN A3 PRECURSOR. TRYPSINGEN A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 TRVLNFNTWIRETMA 258
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HCYQTASRISVRIGEHNIFVTEGTEQRIQASKAIRHPQYNSATI-D-N-DIMLIKLSSPA 117
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                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 41.2%; les 103; Conservative
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244
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AGNATHA (CYCLOSTOMATA).
                                                                                                                                                                  236 SWIASTMAAN 245
                                                                                                                                                                                           250 DWIKKIIGSK 259
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250 DWIKKIIGSK 259
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042159;
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SIGNAL
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                   61
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Matches
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                                                                                                                                                                                                                                                                                                                                                      63 HCYQTASRISVRIGEHNIFVNEGTEQQIQASKALQHPQYNSWTI-D-N-DIMLIKLSSPA 119
                                                                                                                                                                                                                                                                                                                                                                                       120 ILNQYAQAIALPSSCVNTGVMCTISGWGETQTSVGS-PDVLMCVQAPVLSDTSCRNSYPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                       179 DITUNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWGRG-CALPNYPGVYTKVCNYN 237
                                                                                                                                                                                                                                                                                      4 LILALLVGVAAAAPYMYEDHIVGGSECAAHSQPWQVSLNIGYHF-CGGSLINSQWVVSAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 744; DB 12; Length 245;
Pred. No. 1.31e-177;
61; Mismatches 74; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                       3 IFALLVGTA-AAAPYMYEDHIVGGYECAAHSQPWQVSLNIGYHF-CGGSLISSEWVVSAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                         Length 247;
                                                                                                                                                                                                                                       Score 750; DB 12; Length 247
Pred. No. 2.30e-179;
59; Mismatches 77; Indels
                                                                                                                         ROACH J.C.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011899; G2367497; -.
EMBL; AF011352; G2293478; -.
                                                            ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011901; G2367501; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRYPEINOGEN B2 PRECURSOR (FRAGMENT).
PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; PISCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
AGNATHA (CYCLOSTOMATA).
                                                                                                                                                                                       POTENTIAL.
TRYPSIN A3.
6D71AC2E CRC32;
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TRYPSIN B2.
071872F0 CRC32;
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13 PO
245 TR
26001 MW;
                                                                                                                                                                                                               26295 MW;
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                                                                                                                                                                                                                                       set Local Similarity 42.0%;
tches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.3%;
Best Local Similarity 42.0%;
Matches 105; Conservative
                                                                                                SEQUENCE FROM N.A.
TISSUE-ANTERIOR INTESTINE;
                         AGNATHA (CYCLOSTOMATA).
                                                                                                                                                                                         15
247
                                                                                                                                                                                        1
16 2
247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AWIAQTIAAN 247
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                                                  SEQUENCE FROM N.A.
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SIGNAL
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RESULT

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Gaps' 10;
177 DITUNNMICLGYLEGGKDSCQGDSGGPVVCNGQLQGIVSWGRG-CALPNYPGVYTKVCNYN 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLNQYAQAVPLPSSCVGTGVMCTISGWGETQTSVGS-PDVLMCVQAPVLSDTSCRNSYPG 175
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                                                                                                                                      118 TLNQYAQAIPLPSSCVGTGVMCTISGWGETQTSVGS-PDVLMCVQAPVLSDTSCRNSYPG
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Pred. No. 7.44e-176;
63; Mismatches 74; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011900; G2367499; -.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; PISCES;
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TRYPSIN B1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMLLRLTQPAEITDAVQVVELPTQEPEVGSTCLASGWGSIEPENFSYPDDLQCVDLKILP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 IMLLOLRDOASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 KVLEGNEQFINAAKIIRHPKYNR-DTLD-N-DIMLIKLSSPAVINARVSTISLPTAPPAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GTECLISGWGNTLSFGADYPDELKCLDAPVLTQAECKASYPGKITNSMFCVGFLEGGKDS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTAAHCIGDNYQLWLGRHNLFDDEDTAQFVHVSESFPHPCFNMSLLKNHTRQADEDYSHD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GOKCTVSGWGTVTSPRENFPDTLNCAEVKIFPOKKCEDAYPGQITDGMYCAGSSKGA-DT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 QEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKFKTVRLGDHSL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 DDDKIVGGYTCE-NSLPYQVSLNSGSHF-CGGSLISEQWVVSAAHCYKTRIQVRLGEHNI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 WFLVLCLALSLGG-TGAAPPIQSRIVGGWEC---SQPWQAALYHFSTFQCGGILVHPQWV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 WMFLL-L-LG-GAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGWWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 CQRDSGGPVVCNGQLQGVVSWGHG-CAWKNRPGVYTKVYNYVDWIKDTIAANS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPIO HAWADRYAS (HAWADRYAS BABOON).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 259
                                                                                                                                                                                                                                                    m
m
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 710; DB 2; Length 259
Pred. No. 1.12e-167;
51; Mismatches 77; Indels
                                                                                                                                                                                                                                     WIEGAND U., CORBACH S., MINN A., KANG J., MUELLER-HILL GENE 136:167-175(1993).
EMBL; X71345; E74009; -
SEQUENCE 259 AA: Z7983 MW; D2F07A3E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERELYGINA L.M., KAMMERER C.M., HENKEL R.D.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L43121; G871814; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.23e-165;
57; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE KALLIKREIN.
OC5E883F CRC32;
                                                                                                                                                                                                                                                                                                                                                      27983 MW; D2F07A3E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28339 MW;
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01,
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Local Similarity 41.8%;
hes 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLK1.
PAPIO HAMADRYAS (HAMADRYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                   36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.1%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL; SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
KALLIKREIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN 25 ; SEQUENCE 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                        FROM N.A
                                                                                                                                                                                                      MEDLINE; 94123994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q28773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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MEDLINE; 94250683.

MEDLINE; 94250683.

GAUTHIER E.R., DUMAS C., CHAPDELAINE P., TREMBLAY R.R., DUBE J.Y.;
BIOCHIM. BIOPHYS. ACTA 1218:102-104(1994).

-!- CATALYTIC ACTIVITY: PREPERBRIAL CLEAVAGE OF ARG-|-XAA BONDS IN SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE RALLIDIN (LYSYL-BRADYKININ) FROM KININOGENS HYDOLYSES YENDOLYSIS OF MET-|-XAA OR LEU-|-XAA THE RAY ENZYME IS UNUGENS BY CLEAVAGE AT TWO ARG-|-XAA BONDS.

BRADYKININ DIRECTLY FROM AUTOLOGOUS KININOGENS BY CLEAVAGE AT TWO EMBL; X75479; 6414019; -.

SIGNAL; HYDROLASE.
 62 TAAHCINDNYQLWLGRYNLFEHEDTAQFVQVRESFPHPEFNLSLLKNHTRLPEEDYSHDI 121
 122 MLLRLAEPAQITDAVRVLDLPTQEPQVGSTCYASGWGSIEPDKFIYPDDLQCVDLELLSN 181
 182 DICANAHSQKVTEFMLCAGHLEGGKDTCVGDSGGPLICDGVLQGITSWGHVPCGSPNMPA 241
 69
 2 WFLVLCLALSLAGTGAAPPVQSRIIGGWDCTKNSQPWQAALYHYSKFQCGGVLVHPEWVV 61
 Gaps
 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
KALJIRKEIN PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (GLANDULAR KALJIKREIN) (KININOGENIN).
CANIS FAMILIARIS (DOG).
 11;
 TETRAPODA; MAMMALIA;
 CHORDAIA; VERIEBRAIA; IETRAPODA; MAMMALIA;
 36.2%; Score 703; DB 4; Length 261; 40.2%; Pred. No. 1.23e-165;
 Indels
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
 24 POTENTIAL.
261 KALLIKREIN.
28913 MW; 65B49AEF CRC32;
 Mismatches
 261 AA
 239 AA
 KALLIKREIN (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
 01-NOV-1996 (TREMBLREL. 01, CREATED)
 PRT;
 PRT;
 242 VYTKVISHLEWIKETMTAN 260
 01,
 PRELIMINARY;
 PRELIMINARY;
 Local Similarity 40.2%; es 104; Conservative
 063275 PRELIMINAR
063775;
001-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
 241 VYTNICRYLDWIKKIIGSK
 EUTHERIA; CARNIVORA
 EUKARYOTA; METAZOA;
 261 AA;
 EUTHERIA; RODENTIA
 SEQUENCE FROM N.A.
 ₁
 STRAIN-MONGREL
 01-NOV-1996
01-JAN-1998
 SEQUENCE
 Query Match
LT 13
Q29474
Q29474;
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Score 694; DB 10; Length 239;
Pred. No. 5.14e-163;
52; Mismatches 63; Indels 15; Gaps 11;
 ä
 121 TKEPKVGSTCLVSGWGS-TNPSEWEFPDDLQCVNIHLLSNEKCIKAYKEKVTDLMLCAGE 179
 63 SEDV-QHRL-VSQSFRHPDYKPFLMRNHTRKPKDYSNDLMLLHLSEPADITDGVKVIDLP 120
 143 DHCTQPGQKCTVSGWGTVTSPRE-NFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGS 201
 121 TEAVAPIPLPTSCPYGGLSCSVSGWGIAKLGGEAYMPTLLQCLNVPIVDQQVCENTYPGL 180
 ISTIMVCAGYMEGGKDACNGDSGSPLVCDGEVQGLVSWG-QGCAEPNYPGVYVKLCEFHS 239
 64 WYNPYSMQVILGDHNLRVFEGTEQLMKTNTIIWHPSYDYQTL-DF--DIMLIKLYHPVEV 120
 30 EDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQ 89
 6 LLLLIGAAAAVPR-EDGRIIGGYECSPHSRPYMASLNYGYHF-CGGVLINNQWVLSVAHC 63
 CHEN L., DEVRIES A.L., CHENG C.H.;
PROC. NATL. ACAD. SCI. U.S.A. 94:3811-3816(1997).
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-XAA, LYS-|-XAA.
EMBL; U58845; G1399811;
-: EMBL; U58835; G2102686;
-:
 Query Match 34.1%; Score 663; DB 12; Length 249;
Best Local Similarity 41.8%; Pred. No. 5.33e-154;
Matches 104; Conservative 49; Mismatches 86; Indels 10; Gaps
 6 QSRVVGGFKCEKNSQPWQVAVIN-EDL-CGGVLIDPSWVITAAHCYSDNYHVLLGQNNL-
 180 LEGGKDTCRGDSGGPLICDGVLQGITSWGSVPCGEPNKPGIYTKLIKFTSWIKEVM 235
 202 SKGA-DICQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDMIKKII 256
 EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
ACTINOPTERYGII; PERCIFORMES; NOTOTHENIOIDEI; NOTOTHENIIDAE.
 CT 15
092046; 013261; PRELIMINARY; PRT; 249 AA.
092046; 013261; CREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PREPROTRYPSIN PRECURSOR (EC 3.4.21.4) (ALPHA- AND BETA-TRYPSIN).
DISSOSTICHUS MAMSONI. MEMBRADA. OSTEICHTHYES
ZINTZ C.B., MA J.X., CHAO J., CHAO L.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L33840; G609585; -.
 TISSUE-PANCREAS;
CHEN L., DEVRIES A.L., CHENG C.H.C.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
 PROTRYPSIN.
55C59EB4 CRC32;
 0609E3E6 CRC32;
 POTENTIAL
 NON_TER 1 1
SEQUENCE 239 AA; 26382 MW;
 1 15 PH
16 249 PH
249 AA; 27169 MW;
 Query Match
Best Local Similarity 44.9%;
Matches 106; Conservative
 SEQUENCE FROM N.A.
 SIGNAL; HYDROLASE.
 SEQUENCE FROM N.A.
 SEQUENCE
 SIGNAL
 181
 RESULT
1D 099
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